



# STIC Search Report

## Biotech-Chem Library

File Copy  
09/974, 7-60  
updated

STIC Database Tracking Number: 145470

**TO:** David Lamberston  
**Location:** rem/2b79/2c70  
**Art Unit:** 1636  
**Thursday, February 17, 2005**

**Case Serial Number:** 09/974760

**From:** Barb O'Bryen  
**Location:** Biotech-Chem Library  
**Remsen 1A69**  
**Phone:** 571-272-2518

*POB*  
**barbara.obryen@uspto.gov**

### Search Notes

GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: February 15, 2005, 01:46:24 ; Search time 168 Seconds  
 (without alignments)

1079.706 Million cell updates/sec

Title: US-09-974-760B-91  
 Perfect score: 2456  
 Sequence: 1 MAADQGIFTNSVTLSPVEGS.....FSLARKHKGMLRDLNINPP 469

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2105632 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105643

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 95%  
 Listing First 45 summaries

Database : A\_Geneseq\_16Dec04;\*

1: GeneseqP19808;\*  
 2: GeneseqP19808;\*  
 3: GeneseqP20008;\*  
 4: GeneseqP20018;\*  
 5: GeneseqP20028;\*  
 6: GeneseqP20038;\*  
 7: GeneseqP20038;\*  
 8: GeneseqP20048;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

RESULT 1  
 ABR6151  
 ID ABR6151 standard; protein; 469 AA.  
 XX  
 AC ABR6151;  
 XX  
 DT 15-OCT-2003 (first entry)  
 XX  
 DE Aspergillus terreus lovE protein mutant sequence.  
 XX  
 KW LovE; regulator; wild-type; fungus; secondary metabolite; lovastatin;  
 KW food additive; vitamin; mutant; mutein.  
 XX  
 OS Aspergillus terreus.

XX  
 Key Location/Qualifiers  
 FT Misc-difference 4  
 /note= "ASP at this position in wild type protein"  
 FT Misc-difference 9  
 /note= "Thr at this position in wild type protein"  
 FT Misc-difference 14  
 /note= "Leu at this position in wild type protein"  
 FT Misc-difference 16  
 /note= "Pro at this position in wild type protein"  
 FT Misc-difference 18  
 /note= "Glu at this position in wild type protein"  
 FT Misc-difference 21  
 /note= "Arg at this position in wild type protein"  
 FT Misc-difference 23  
 /note= "Gly at this position in wild type protein"  
 FT Misc-difference 31  
 /note= "Phe at this position in wild type protein"  
 FT Misc-difference 34  
 /note= "Ser at this position in wild type protein"  
 FT Misc-difference 41  
 /note= "Gln at this position in wild type protein"  
 FT Misc-difference 43  
 /note= "Ile at this position in wild type protein"  
 FT Misc-difference 46  
 /note= "Thr at this position in wild type protein"  
 FT Misc-difference 62  
 /note= "Gln at this position in wild type protein"  
 FT Misc-difference 73  
 /note= "Cys at this position in wild type protein"  
 FT Misc-difference 77  
 /note= "Lys at this position in wild type protein"  
 FT Misc-difference 80  
 /note= "Gln at this position in wild type protein"  
 FT

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2035	82.9	469	6 ABR6151	Aspergillus terreus lovE protein mutant sequence.
2	830	33.8	459	5 AAU10871	Aspergillus terreus lovE protein mutant sequence.
3	830	33.8	459	7 ADE81191	Aspergillus terreus lovE protein mutant sequence.
4	157.5	6.4	424	5 ABP6135	Aspergillus terreus lovE protein mutant sequence.
5	157.5	6.4	424	5 ABP35719	Aspergillus terreus lovE protein mutant sequence.
6	154.5	6.3	919	5 ABP35687	Aspergillus terreus lovE protein mutant sequence.
7	154.5	6.3	919	8 ADR43829	Aspergillus terreus lovE protein mutant sequence.
8	141	5.7	727	7 ADC52108	Aspergillus terreus lovE protein mutant sequence.
9	136	5.5	604	2 AAW37163	Aspergillus terreus lovE protein mutant sequence.
10	136	5.5	604	5 ABP35591	Aspergillus terreus lovE protein mutant sequence.
11	135	5.5	433	5 ABP35583	Aspergillus terreus lovE protein mutant sequence.
12	132	5.4	1170	5 ABP35667	Aspergillus terreus lovE protein mutant sequence.
13	132	5.4	1170	8 AAW3829	Aspergillus terreus lovE protein mutant sequence.
14	131.5	5.4	480	5 ABP35612	Aspergillus terreus lovE protein mutant sequence.
15	130.5	5.3	662	5 ABP35590	Aspergillus terreus lovE protein mutant sequence.
16	130.5	5.3	792	5 ABG93477	Aspergillus terreus lovE protein mutant sequence.
17	129.5	5.3	579	5 ABP35589	Aspergillus terreus lovE protein mutant sequence.
18	126.5	5.2	341	2 AAW58573	Aspergillus terreus lovE protein mutant sequence.
19	126	5.1	821	5 ABG93475	Aspergillus terreus lovE protein mutant sequence.
20	124.5	5.1	736	5 ABP35614	Aspergillus terreus lovE protein mutant sequence.
21	124	5.0	984	5 ABP35627	Aspergillus terreus lovE protein mutant sequence.
22	123.5	5.0	437	5 ABP35582	Aspergillus terreus lovE protein mutant sequence.
23	123.5	5.0	607	5 ABP35705	Aspergillus terreus lovE protein mutant sequence.
24	122	5.0	821	5 ABG93469	Aspergillus terreus lovE protein mutant sequence.
25	122	5.0	821	5 ABP35586	Aspergillus terreus lovE protein mutant sequence.

Result No.	Score	Query	Match	Length	DB ID	Description
1	157.5	6.4	424	4	US-10-029-180-104	Sequence 100, App
2	136	5.5	604	3	US-09-197-814-3	Sequence 3, App
3	136	5.5	604	4	US-09-920-581-3	Sequence 3, App
4	119	4.8	631	3	US-09-147-119-7	Sequence 7, App
5	119	4.8	707	4	US-09-949-016-0495	Sequence 845, App
6	118	4.8	439	4	US-09-248-796A-18964	Sequence 1864, App
7	116	4.7	989	4	US-09-248-796A-19109	Sequence 1909, App
8	112.5	4.6	685	4	US-09-248-796A-20197	Sequence 20197, App
9	111	4.5	986	4	US-09-248-796A-19088	Sequence 1988, App
10	109	4.4	534	4	US-09-248-796A-19568	Sequence 19568, App
11	108.5	4.4	314	4	US-09-248-796A-18676	Sequence 18676, App
12	108	4.4	835	4	US-09-252-991A-32121	Sequence 3221, App
13	102.5	4.2	479	4	US-09-248-796A-17550	Sequence 17560, App
14	106.5	4.3	775	2	US-08-714-070A-1	Sequence 1, App
15	105	4.3	971	4	US-09-248-796A-19531	Sequence 19331, App
16	104	4.2	335	4	US-09-248-796A-17099	Sequence 17099, App
17	104	4.2	1341	4	US-09-949-016-6890	Sequence 6890, App
18	104	4.2	1344	4	US-09-949-016-10925	Sequence 10225, App
19	102.5	4.2	808	4	US-09-248-796A-18679	Sequence 18679, App
20	101.5	4.1	351	4	US-09-248-796A-20887	Sequence 20887, App
21	101	4.1	421	4	US-09-248-796A-19591	Sequence 19591, App
22	101	4.1	515	4	US-09-252-991A-22451	Sequence 22451, App
23	101	4.1	1587	4	US-09-845-593A-10	Sequence 10, App
24	101	4.1	1587	4	US-09-561-109B-3	Sequence 3, App
25	100	4.1	758	4	US-10-029-180-92	Sequence 92, App
26	99	4.0	1065	4	US-09-538-092-84	Sequence 84, App
27	98.5	4.0	309	4	US-10-029-180-98	Sequence 98, App

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OM protein - protein search, using sw model

Run on: February 15, 2005, 02:03:56 ; Search time 133 Seconds (without alignments)

1152.221 Million cell updates/sec

Title: US-09-974-760b-91

Perfect score: 2456

Sequence: 1 MADQGIFTNSVTLSPVTEGS . . . . . FSLARKXHKHGMRLDNIPP 469

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376809

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 95% Listing first 45 summaries

Database : Published Applications AA: \*

1: /cgn2\_6/ptodata/2/pubpaas/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaas/PCT\* NEW PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaas/US06 NEW PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaas/US05 PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaas/US04 PUBCOMB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaas/PCT\* NEW PUB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaas/US03 PUBCOMB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaas/US02 NEW PUB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaas/US01 PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaas/US09B PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaas/US09C PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaas/US09 NEW PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaas/US10A PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaas/US10B PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaas/US10C PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaas/US10D PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaas/US10 NEW PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaas/US11 NEW PUB.pep:\*

19: /cgn2\_6/ptodata/2/pubpaas/US60 NEW PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubpaas/US60 PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1858.5	75.7	366	16	US-10-402-056-105	Sequence 105, App
2	810	33.8	459	10	US-09-836-705-42	Sequence 42, App
3	157.5	6.4	424	13	US-10-029-180-104	Sequence 104, App
4	157.5	6.4	424	15	US-10-149-310-302	Sequence 302, App
5	154.5	6.3	919	15	US-10-359-493-1435	Sequence 1435, App
6	154.5	6.3	919	15	US-10-149-310-238	Sequence 238, App
7	136	5.5	604	9	US-09-920-581-3	Sequence 3, App
8	136	5.5	604	14	US-10-371-421-3	Sequence 46, App
9	136	5.5	604	15	US-10-149-310-46	Sequence 38, App
10	135	5.5	433	9	US-09-801-368-18	Sequence 30, App
11	135	5.5	433	15	US-10-149-310-30	Sequence 2259, App
12	132	5.4	1170	15	US-10-359-493-22259	Sequence 198, App
13	132	5.4	1170	15	US-10-149-310-198	Sequence 284, App

RESULT 1  
US-10-402-056-105  
Sequence 105, Application US/10402056  
; Publication No. US20040191877A1  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, Shannon  
; APPICANT: Sherman, Amir  
; APPICANT: Trueheart, Jo Joshua  
; APPICANT: Milne, G. Todd  
; TITLE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES  
; FILE REFERENCE: 14184-029001  
; CURRENT APPLICATION NUMBER: US/10/402.056  
; CURRENT FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: PCT/US02/32248  
; PRIOR FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US 09/974,760  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US 60/328,339  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 105  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetically generated variant

Query Match 75.7%; Score 1858.5; DB 16; Length 366;  
Best Local Similarity 77.6%; Pred. No. 1.4e-159;  
Matches 364; Conservative 1; Mismatches 1; Indels 103; Gaps 1;  
US-10-402-056-105  
Qy 1 MAADQGIFTNSVTLSPIVEGSTGGTLPRAFRSCDRCHAOKTKCTGNKEVTCORC 60  
Db 1 MAADQGIFTNSVTLSPIVEGSTGGTLPRAFRSCDRCLAQKTKCTGNKEVTCORC 60

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 15, 2005, 01:55:19 (without alignments)  
1128.142 Million cell updates/sec

Title: US-09-974-760B-91  
Perfect score: 2456  
Sequence: 1 MAADQGIFTNSVTLSPVEGS.....FSLARIGHGMRLDINNIPP 469

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 95%

Listing First 45 summaries

Database : PIR 79.1

1: Pir1;\*

2: Pir2;\*

3: Pir3;\*

4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154.5	6.3	919	2 S45889	probable regulator
2	136.1	5.5	604	2 JC7252	transcription acti
3	135	5.5	433	2 S69999	sterigmatocystin s
4	132	5.4	1170	2 S30010	probable finger pr
5	131.5	5.4	480	2 T38582	hypothetical funga
6	124.5	5.1	768	2 T37601	probable transcript
7	123.5	5.0	607	2 S63395	probable membrane
8	121.5	4.9	964	2 S48404	probable membrane
9	121	4.9	470	2 S58826	hypothetical prote
10	119	4.8	648	2 T20144	probable transcript
11	118.5	4.8	857	2 T40824	regulatory protein
12	117	4.8	473	1 RGYM3	probable zinc-fing
13	116.5	4.8	767	2 T41344	CAT8 protein - yea
14	116.5	4.7	1445	2 T14913	polyketide synthas
15	115	4.7	6420	2 T30283	transcription acti
16	113.5	4.6	650	2 JC7937	zinc finger transci
17	110.5	4.5	827	2 T39608	hypothetical prote
18	110	4.5	909	2 T06635	nucleoporin - frui
19	109	4.4	1349	2 T13031	nucleoporin 154 -
20	109	4.4	1365	2 T13991	thiamin repressible
21	106.5	4.3	775	2 S41962	hypothetical zinc-
22	106.5	4.3	867	2 T41308	microtubule-associ
23	106.5	4.3	5327	2 T13564	hypothetical prote
24	106	4.3	743	2 T40521	CAT8 protein - yea
25	106	4.3	1433	2 S54587	230k bullous pemph
26	105	4.3	997	2 A60776	K1A0637 protein -
27	104.5	4.3	1171	2 T00380	hypothetical prote
28	104	4.2	1280	2 T00365	hypothetical prote
29	104	4.2	1587	2 GB6467	hypothetical prote

#### RESULT 1

S45889

probable regulatory protein YBR033w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YBR0318

C;Species: Saccharomyces cerevisiae

C;Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 16-Aug-2004

C;Accession: S45889; S46562

R;Grivell, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.

submitted to the Protein Sequence Database, August 1994

A;Reference number: S45875

A;Accession: S45889

A;Molecule type: DNA

A;Residues: 1-919 <GRI>

A;Cross references: UNIPROT:P38073; EMBL:235902; PIDN:CAA84975.1; PID:9536247

N;Experimental source: strain S288C

R;Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.

Year 10 (Suppl. A), S75-S80, 1994

A;Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II f

lly identified genes and a homologue of the SC01 gene.

A;Reference number: S46551; PMID:8091864

A;Accession: S46562

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-919 <SMI>

A;Cross references: ENB:X76078; NID:9498748; PIDN:CAA55688.1; PID:9498760

A;Experimental source: strain S288C

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993

C;Genetics:

A;Cross references: SGD:S0000237

A;Map position: 2R

A;Note: YBR033w

C;Superfamily: GAL4 zinc binuclear cluster homology

C;Keywords: DNA binding; transmembrane protein; zinc finger

F;21-90/Domain: GAL4 zinc binuclear cluster homology <GAL4>

F;56-85/Domain: zinc finger

F;408-44/Domain: transmembrane #status Predicted <TM1>

F;1482-504/Domain: transmembrane #status Predicted <TM2>

F;547-563/Domain: transmembrane #status Predicted <TM3>

F;703-740/Domain: transmembrane #status Predicted <TM4>

F;790-806/Domain: transmembrane #status Predicted <TM5>

Query Match 6.3%; Score 154.5; DB 2; Length 919;

Best Local Similarity 23.1%; Pred. No. 0.0012; Mismatches 52; Gaps 142;

Matches 82; Conservative 52; Gaps 79; Gaps 14;

QY 2 AADQGIFTNSVTLSPVEGSRTGTTPLPRAFRSCDRCHAQKIKCTGKKEVTGAPCQRCQ 61

Db 23 SAGNGEVNQSVSSRNCGSERGKQKASHADQCRKRKFDKH-TG-vcQGCL 79

QY 62 QAGIRC---VYSERCPKRKLROSRAADLVSAPP-----CL 95

Db 80 EVGEKCGQFTRVPLKRGPAKRGSVSIEKFQSSNDPLOYRPRTHSYPMNSGNLYPLSLAR 139

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 15, 2005, 01:47:14 ; Search time 173 Seconds  
(without alignments)  
1388.238 Million cell updates/sec

Title: US-09-974-760B-91

Perfect score: 2456

Sequence: 1 MADQGIFTNTSVTLPVVEGS.....FSLARKHKGMLRDLNIPP 469

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612377

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

POST-processing: Minimum Match 0%

Maximum Match 95%

Listing first 45 summaries

Database : UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	830	33.8	459	2	Q8J0F2	OBj0f2 penicillium	
2	161.5	6.6	1010	2	Q7S6Q4	Q7s6q4 neurospora	
3	158	6.4	478	2	Q6BPX4	Q6bpX4 debaryomyce	
4	154.5	6.3	919	1	YBO3 YEAST	P38073 saccharomyce	
5	148.5	6.0	500	2	Q6Q877	Q6q877 leptocephaly	
6	145.5	5.9	1082	2	Q6CXE0	Q6cx00 kluveromyce	
7	145	5.9	603	2	Q7SEM4	Q7sem4 neurospora	
8	142.5	5.8	520	2	Q8X0T1	Q8x0t1 neurospora	
9	138.5	5.6	554	2	Q7SAV4	Q7sav4 neurospora	
10	137	5.6	1287	2	Q6FLP2	Q6flp2 candida gla	
11	136	5.5	604	2	Q6D201	Q6d201 aspergillus	
12	135.5	5.5	442	2	Q8TGB1	Q8tgb1 emericella	
13	135	5.5	433	1	AFLR EMEINI	P52957 emericella	
14	133	5.4	922	2	Q6FX18	Q6fx18 candida gla	
15	133.5	5.4	1254	2	Q6FJW6	Q6fjw6 candida gla	
16	133	5.4	470	2	Q9UVH4	Q9uvh4 saccharomyce	
17	132	5.4	1170	1	YKD8 YEAST	P32862 saccharomyce	
18	131.5	5.4	480	2	Q94392	Q94392 schizosacch	
19	130.5	5.3	662	2	Q9Y728	Q9y728 emericella	
20	130.5	5.3	785	2	Q677V8	Q677v8 aspergillus	
21	130	5.3	436	2	Q6IWFS3	Q6iwf3 aspergillus	
22	129.5	5.3	579	2	Q9Y8A1	Q9y8a1 aspergillus	
23	128.5	5.2	442	2	Q8TG77	Q8tg77 aspergillus	
24	128.5	5.2	442	2	Q8TG79	Q8tg79 aspergillus	
25	128.5	5.2	442	2	Q8TG84	Q8tg84 aspergillus	
26	128	5.2	832	2	Q6FUL5	Q6ful5 candida gla	
27	126.5	5.2	341	1	ACE2 TRIRE	Q96vng6 trichoderma	
28	126.5	5.2	442	2	Q8TFC7	Q8tfc7 aspergillus	
29	126.5	5.2	442	2	Q8TG78	Q8tg78 aspergillus	
30	126.5	5.2	442	2	Q8TG86	Q8tg86 aspergillus	
31	126.5	5.2	1353	2	Q7S6K8	Q7s6k8 neurospora	

## ALIGNMENTS

32	125.5	5.1	442	2	Q8TG92	Q8tg92 aspergillus
33	124.5	5.1	442	2	Q8TG93	Q8tg93 aspergillus
34	124.5	5.1	442	2	Q8TG87	Q8tg87 aspergillus
35	124	5.0	984	2	Q94167	Q94167 glomerella
36	123.5	5.0	444	2	AFLR ASPFL	P41165 aspergillus
37	123.5	5.0	607	1	Q8TG71	Q8tg71 aspergillus
38	123.5	5.0	444	2	YN92 YEAST	P53749 saccharomyce
39	123	5.0	444	2	Q8TG72	Q8tg72 aspergillus
40	122	5.0	441	2	Q8TG80	Q8tg80 aspergillus
41	122	5.0	444	2	Q8JYV0	Q8jyv0 aspergillus
42	122	5.0	444	2	Q87AB8	Q87ab8 aspergillus
43	122	5.0	821	1	ALCR EMEINI	P21228 emericella
44	121.5	4.9	964	1	YINO YEAST	P40467 saccharomyce
45	121	4.9	444	2	Q8TFC9	Q8tfc9 aspergillus

RESULT 1  
Q8J0F2 ID  
PRELIMINARY; PRT; 459 AA.

AC Q8J0F2; 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Transcription factor.

GN Name=mICR;

OS Eubaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

OX NCBI\_TaxID=5077;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-2216865; PubMed=12172803; DOI=10.1007/s00438-002-0697-y;

RX Abe Y., Suzuki T., Ono C., Iwamoto K., Hosobuchi M., Yoshioka H.,

RT "Molecular cloning and characterization of an ML-236B (compactin)"

RT biosynthetic gene cluster in Penicillium citrinum.";

RT Mol. Genet. Genomics 267:636-646(2002).

RN [12]

RP SEQUENCE FROM N.A.

RX MEDLINE-22227327; PubMed=12242508; DOI=10.1007/s00438-002-0736-8;

RA Abe Y., Suzuki T., Mizuno T., Ono C., Iwamoto K., Hosobuchi M.,

RA Yoshioka H.,

RA "Effect of increased dosage of the ML-236B (compactin) biosynthetic gene cluster on ML-236B production in Penicillium citrinum.";

RT gene cluster on ML-236B production in Penicillium citrinum.";

RL Mol. Genet. Genomics 268:130-137(2002).

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster.

CC domain.

DR EMBL; AB072893; BAC20569.1; -;

DR GO:GO-0005634; C:nucleus; IEA.

DR GO:GO-0003700; F:transcription factor activity; IEA.

DR GO:GO-0008210; F:zinc finger binding; IEA.

DR GO:GO-0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR001138; Fungi\_Trcsp\_N.

DR Pfam; PF00172; Zn\_fus; 1.

DR PRINTS; PRO0054; FUNGALNZCS.

DR SMART; SM0066; GAL4.

DR PROSITE; PS00463; ZN2\_CY6\_FUNGAL\_1; UNKNOWN\_1.

DR PROSITE; PS0048; ZN2\_CY6\_FUNGAL\_2; 1.

KW DNA-binding; Metal-binding; Nuclear protein.

KW Transcription regulation; Zinc.

SO SEQUENCE 459 AA; 50356 MW; 4D2D1B33078F46C1 CRC64;

DR SHRT; SM0066; GAL4.

DR PROSITE; PS00463; ZN2\_CY6\_FUNGAL\_1; UNKNOWN\_1.

Query Match Score 33.8%; Pred. No. 3.3e-54;

Best Local Similarity 42.2%; Mismatches 153;

Matches 196; Conservative 62; Gaps 54;

Indels 5

Gaps 9;

Db 26 LPRRAFRSCDCRHAQKIKTCGKVEYGRAPFCQOAGLRCVYSERCPKRLQKRSRA- 84

Db 12 LRRRAFRSCDCRHAQKLKTCGNSANLVRQCRQOAGLRCVYSERUPKRNJHKEARAG 71

Result No.	Score	Query	Match	Length	DB	ID	Description	FEATURES	Source						
1	830	33.8	1380	6	BD178141	On the st	BD178141 On the st	PN	29-OCT-2002						
C 2	811	33.0	34203	6	BD178102	On the st	BD178102 On the st	PP	18-APR-2001						
C 3	811	33.0	34203	6	BD178103	On the st	BD178103 On the st	PI	18-APR-2001						
C 4	811	33.0	34203	6	BD013765	ML-236B b	BD013765 ML-236B b	PC	(C12P17/06,C2R1-80),C2N15/00						
Copyright (c) 1993 - 2005 Compugen Ltd.															
OM protein - nucleic search, using frame_plus_p2n model															
Run on:	February 16, 2005, 20:20:52 ;	Search time 51.00	Seconds	4455.980 Million cell updates/sec											
Title:	US-09-974-760B-91														
Perfect score:	2456														
Sequence:	1 MADQGIFTNSVTLSPVEGS . . . . . FSLARKHKGMDLNNIPP 469														
Scoring table:	BLOSUM62														
Xgapext	0.5														
Ygapext	0.5														
Fgapext	0.5														
DelOp	7.0														
	6.0														
Searched:	4702333 seqs,	24227607935 residues													
Total number of hits satisfying chosen parameters:	9416463														
Minimum DB seq length:	0														
Maximum DB seq length:	2000000000														
Post-processing: Minimum Match 0%															
Post-processing: Maximum Match 95%															
Listing first 45 summaries															
Command line Parameters:															
-MODEL=frame+ p2n model -DEV=11P															
-Q=-cgn2_1 /USARIO spoil_p10_query_560/runat_14022005_160342_6751/app_query.fasta_1.647															
-DB=denEmb1 -QFM=1 -SPAT=fastap -SUFIX=9pct,rgc -MINMATCH=0.1 -LOOPEXT=0															
-UNITS=bits -SPART=1 -END=-1 -MATRIX=b1:GCGUM62 -TRANS=human10_cdi -LIST=45															
-DOCALIGN=200 -THR SCORE=9PCT -THR MAX=95 THR MIN=0 -ALIGN=15 -NODE=LOCAL															
-OUTFMT=pio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=0 -NODE=00000000															
-USR=US0974760 @CCIN 1.5600 @runat 14022005_160342_6751 -NCPU=6 -ICPU=3															
-NO_MMAPP -LARGEQUERY -NEG SCORES=0 WAIT=100 -DSBLLOCK=100 -LONGLOG															
-DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -LONGLOG															
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7															
Database :															
GenEmbl:	*														
1: gb_ba:*															
2: gb_ng:*															
3: gb_in:*															
4: gb_om:*															
5: gb_ov:*															
6: gb_dat:*															
7: gb Dh:*															
8: gb_Dp:*															
9: gb_Dr:*															
10: gb_ro:*															
11: gb_stb:*															
12: gb_sy:*															
13: gb_un:*															
14: gb_i:*															
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the results being printed.															
SUMMARIES															
Result No.	Score	Query	Match	Length	DB	ID	Description	FEATURES	Source						
1	830	33.8	1380	6	BD178141	On the st	BD178141 On the st	PN	29-OCT-2002						
C 2	811	33.0	34203	6	BD178102	On the st	BD178102 On the st	PP	18-APR-2001						
C 3	811	33.0	34203	6	BD178103	On the st	BD178103 On the st	PI	18-APR-2001						
C 4	811	33.0	34203	6	BD013765	ML-236B b	BD013765 ML-236B b	PC	(C12P17/06,C2R1-80),C2N15/00						
Copyright (c) 1993 - 2005 Compugen Ltd.															
OM protein - nucleic search, using frame_plus_p2n model															
Run on:	February 16, 2005, 20:20:52 ;	Search time 51.00	Seconds	(without alignments)											
Title:	US-09-974-760B-91														
Perfect score:	2456														
Sequence:	1 MADQGIFTNSVTLSPVEGS . . . . . FSLARKHKGMDLNNIPP 469														
Scoring table:	BLOSUM62														
Xgapext	0.5														
Ygapext	0.5														
Fgapext	0.5														
DelOp	7.0														
	6.0														
Searched:	4702333 seqs,	24227607935 residues													
Total number of hits satisfying chosen parameters:	9416463														
Minimum DB seq length:	0														
Maximum DB seq length:	2000000000														
Post-processing: Minimum Match 0%															
Post-processing: Maximum Match 95%															
Listing first 45 summaries															
Command line Parameters:															
-MODEL=frame+ p2n model -DEV=11P															
-Q=-cgn2_1 /USARIO spoil_p10_query_560/runat_14022005_160342_6751/app_query.fasta_1.647															
-DB=denEmb1 -QFM=1 -SPAT=fastap -SUFIX=9pct,rgc -MINMATCH=0.1 -LOOPEXT=0															
-UNITS=bits -SPART=1 -END=-1 -MATRIX=b1:GCGUM62 -TRANS=human10_cdi -LIST=45															
-DOCALIGN=200 -THR SCORE=9PCT -THR MAX=95 THR MIN=0 -ALIGN=15 -NODE=LOCAL															
-OUTFMT=pio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=0 -NODE=00000000															
-USR=US0974760 @CCIN 1.5600 @runat 14022005_160342_6751 -NCPU=6 -ICPU=3															
-NO_MMAPP -LARGEQUERY -NEG SCORES=0 WAIT=100 -DSBLLOCK=100 -LONGLOG															
-DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -LONGLOG															
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7															
Database :															
GenEmbl:	*														
1: gb_ba:*															
2: gb_ng:*															
3: gb_in:*															
4: gb_om:*															
5: gb_ov:*															
6: gb_dat:*															
7: gb_Dh:*															
8: gb_Dp:*															
9: gb_Dr:*															
10: gb_ro:*															
11: gb_stb:*															
12: gb_sy:*															
13: gb_un:*															
14: gb_i:*															
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the results being printed.															
SUMMARIES															
Result No.	Score	Query	Match	Length	DB	ID	Description	FEATURES	Source						
1	830	33.8	1380	6	BD178141	On the st	BD178141 On the st	PN	29-OCT-2002						
C 2	811	33.0	34203	6	BD178102	On the st	BD178102 On the st	PP	18-APR-2001						
C 3	811	33.0	34203	6	BD178103	On the st	BD178103 On the st	PI	18-APR-2001						
C 4	811	33.0	34203	6	BD013765	ML-236B b	BD013765 ML-236B b	PC	(C12P17/06,C2R1-80),C2N15/00						
Copyright (c) 1993 - 2005 Compugen Ltd.															
OM protein - nucleic search, using frame_plus_p2n model															
Run on:	February 16, 2005, 20:20:52 ;	Search time 51.00	Seconds	(without alignments)											
Title:	US-09-974-760B-91														
Perfect score:	2456														
Sequence:	1 MADQGIFTNSVTLSPVEGS . . . . . FSLARKHKGMDLNNIPP 469														
Scoring table:	BLOSUM62														
Xgapext	0.5		</												

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 16, 2005, 19:56:52 (without alignments)  
Perfect score: 4317.821 Million cell updates/sec

Title: US-09-974-760B-91  
Sequence: 1 MADQG1PTNSVTLSPVEGS.....FSLARKXHKHGMRLDNIPP 469

Scoring table: BLOSUM62  
Xgapop 10.0 Xgapext 0.5  
Ygapop 10.0 Ygapext 0.5  
Egapop 6.0 Egapext 7.0  
Deiop 6.0 Delext 7.0

Searched: 4390206 seqs, 2953870667 residues

Total number of hits satisfying chosen parameters: 87803 82

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 95%  
Listing first 45 summaries

Command line parameters:

```

-MODEL=Frame+ p2n.model -DEVA=1p
-Q=cgn2_1/USP01_spool1 -P=USP0974760 -DB=UNI_GenSeq_1.6.47
-SUFFIX=95pct.rng -LOOPEXT=0 -QMT=Fatap -START=1 -END=1 -UNITS=bits -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-1.05 -DOALIGN=200 -THR SCORE=DCT -THR MAX=95 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORMEXT -HEAPSIZE=100 -MINLEN=0 -MAXLEN=2000000000
-USR=USP0974760 @CCN 1.1 708 @runat 14022005 160342 6744 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NSEQ SCORES=0 WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAFEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

Database : N\_GenSeq\_16Dec04:\*

1: geneseqm1980s:\*

2: geneseqm1990s:\*

3: geneseqm2000s:\*

4: geneseqm2001as:\*

5: geneseqm2001bs:\*

6: geneseqm2002as:\*

7: geneseqm2002bs:\*

8: geneseqm2003as:\*

9: geneseqm2003bs:\*

10: geneseqm2003cs:\*

11: geneseqm2003ds:\*

12: geneseqm2004as:\*

13: geneseqm2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	830	31.8	1377	10	ADE81190	Ade81190 Mlcr codi
2	830	31.8	1380	6	AAS16808	AAS16808 Penicilli
C 3	811	33.0	34203	4	AAF74546	AAF74546 Penicilli
C 4	811	33.0	34203	6	AAS16770	AAS16770 Penicilli
C 5	811	33.0	34263	4	AAF74547	AAF74547 Penicilli

## ALIGNMENTS

RESULT 1	Location/Qualifiers
AD881190	ID ADE81190 standard; DNA; 1377 BP.
XX	
AC	AD881190;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Mlcr coding sequence, SEQ ID 18.
XX	
KW	ML-236B; HMG-CoA reducing enzyme; ds; Mlcr.
XX	
OS	Penicillium citrinum.
XX	
PN	JP2003116567-A.
XX	
FH	
Key CDS	1..1377
FT	/*tag= a
FT	/product= "Mlcr"
XX	

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 16, 2005, 21:08:47 ; Search time 234 Seconds  
(without alignments)

3279.546 Million cell updates/sec

Title: US-09-974-760B-91  
Perfect score: 2456  
Sequence: 1 MADQGIFTNSVTLSPVVEGS.....PSLARKXKHGMLRLDNNIPP 469

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop. 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405566

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95\*, Maximum Match 95\*, Listing First 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xml
-Q=1 -DB=issued -P=US0974760/runat14022005_160343_6778/app_query.fasta_1.647
-DB_ISSUED_PATENTS_NA -QFORMAT=fastaP -SUFFIX=5pct.rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=518 -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCAIGN=200 -THR SCORE=95 -THR MAX=95 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFORMAT=pto -NORM=ext -HEAISIGN=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09974760 @CGN_1_1_105 @runat14022005_160343_6778 -NCRU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMEOUT=30 -WARN TIMEOUT=10 -DELEXT=7 -XGAPEXT=0.5 -FGAPEXT=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Issued Patents NA:\*

```
1: /cggn2_6/podata/1/ina/5A.COMB.seq/*
2: /cggn2_6/podata/1/ina/5B.COMB.seq/*
3: /cggn2_6/podata/1/ina/6A.COMB.seq/*
4: /cggn2_6/podata/1/ina/6B.COMB.seq/*
5: /cggn2_6/podata/1/ina/PCUTUS.COMB.seq/*
6: /cggn2_6/podata/1/ina/backfile1.seq/*
```

Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	157.5	6.4	1272	4 US-10-029-180-103	Sequence 103, App
2	139	5.7	3980	3 US-09-197-014-1	Sequence 1, Appli
3	139	5.7	3980	4 US-09-920-581-1	Sequence 2, Appli
4	139	5.7	3980	4 US-09-920-581-2	Sequence 2, Appli
5	129.5	5.3	49225	4 US-09-902-040-1269	Sequence 1269, Ap
6	129.5	5.2	2844	4 US-09-669-980-A-5	Sequence 5, Appli
7	129.5	5.2	3061	3 US-09-147-119-6	Sequence 6, Appli
8	126.5	5.2	3061	3 US-09-147-119-6	Sequence 6, Appli
9	126.5	5.2	3145	4 US-09-949-016-2624	Sequence 2624, Ap
10	121.5	4.9	2970	4 US-09-248-793-A-5006	Sequence 5006, Ap
11	121	4.9	110585	4 US-09-949-016-13427	Sequence 13427, A
12	119.5	4.9	4403765	3 US-09-103-840-A-2	Sequence 2, Appli

Sequence 1, Appli  
Sequence 1465, App  
Sequence 97, Appli  
Sequence 4881, App  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 146, Appli  
Sequence 4905, App  
Sequence 10, Appli  
Sequence 10, Appli  
Sequence 6034, App  
Sequence 1019, App  
Sequence 5054, App  
Sequence 12761, A  
Sequence 16796, A  
Sequence 13525, A  
Sequence 7, Appli  
Sequence 1, Appli  
Sequence 15292, A  
Sequence 49, Appli  
Sequence 11431, A  
Sequence 936, App  
Sequence 5880, App  
Sequence 5165, App  
Sequence 3, Appli  
Sequence 4573, App  
Sequence 12103, A  
Sequence 792, App  
Sequence 15670, A  
Sequence 15550, A  
Sequence 7588, App  
Sequence 775, App  
Sequence 743, App  
Sequence 989, App

ALIGNMENTS

RESULT 1	US-10-019-180-103	Sequence 103, Application US/10029180 ; GENERAL INFORMATION: ; APPLICANT: Cali, Brian M. ; APPLICANT: Holtzman, Doug ; APPLICANT: Maddsen, Kevin T. ; APPLICANT: Milna, G. Todd ; APPLICANT: Sherman, Amir ; APPLICANT: Silva, Jeffry C. ; APPLICANT: Trueheart, Josh ; APPLICANT: Zhang, Lixin ; TITLE OF INVENTION: No. 6806082e1 Regulators of Fungal Gene Expression ; FILE REFERENCE: MIC-004 ; CURRENT FILING DATE: 2001-12-22 ; PRIOR APPLICATION NUMBER: US 60/257,431 ; PRIOR FILING DATE: 2000-12-22 ; NUMBER OF SEQ ID NOS: 138 ; SOFTWARE: Fast-SEQ for Windows Version 4.0 ; SEQ ID NO: 103 ; LENGTH: 1272 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: fungal gene ; US-10-029-180-103
1	Sequence 103, App	
2	Sequence 1, Appli	
3	Sequence 2, Appli	
4	Sequence 2, Appli	
5	Sequence 1269, Ap	
6	Sequence 5, Appli	
7	Sequence 6, Appli	
8	Sequence 6, Appli	
9	Sequence 2624, Ap	
10	Sequence 5006, Ap	
11	Sequence 13427, A	
12	Sequence 2, Appli	

Conservative: 67  
Mismatch: 170  
Indels: 111  
Gaps: 19

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 16, 2005, 22:54:23 ; Search time 673 Seconds

(without alignments)

4111.910 Million cell updates/sec

Title: US-09-974-760b-91

Perfect score: 2456

Sequence: 1 MADQGIFTNSTVTLSPVEGS . . . . . FSLARKXKHGMLRDLNNIPP 469

Scoring table: BLOSUM62

Xgapext 10.0 / Xgapext 0.5

Ygapext 10.0 / Ygapext 0.5

Fgapext 6.0 / Fgapext 7.0

DelOp 6.0 / Delext 7.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757281

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 95%

Listing First 45 summaries

Command line parameters:

```
-MODEL=frame+ p2n.model -DEV=>1P
-Q= /cgn2_1 /USP0 spooll P/09374760/runat 14022005_160344_5868/app_query_fasta_1.647
-DB=EPPublished_Applications_NA -QFMT=fastaP -SUFFIX=95pct.rnpb -MINMATCH=0.1
-LOOPCPL=0 -LOOPBEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=DIOSum62
-TRANS=human40_cdi -LIST=45 -DOCALLIGN=20 -THR SCORE=pct -THR MAX=95
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER:US09374760 @CGN_1_723 @runat 14022005_160344_6868
-NCPU=6 -NCPU=3 -NO_MMAP -LARGE_QUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5
-FGAPPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database :

Published Applications NA:\*

1: /cgn2\_6/prodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/prodata/2/pubpna/US05\_PUBCOMB.seq:\*

5: /cgn2\_6/prodata/2/pubpna/US04\_PUBCOMB.seq:\*

6: /cgn2\_6/prodata/2/pubpna/PCUTS\_PUBCOMB.seq:\*

7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/prodata/2/pubpna/US09\_PUBCOMB.seq:\*

9: /cgn2\_6/prodata/2/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq:\*

14: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq:\*

17: /cgn2\_6/prodata/2/pubpna/US10F\_PUBCOMB.seq:\*

18: /cgn2\_6/prodata/2/pubpna/US10G\_PUBCOMB.seq:\*

19: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*

20: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq:\*

21: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*

22: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

## ALIGNMENTS

RESULT 1  
US-10-402-056-114

Sequence 114, Application US/10402056

; Publication No. US2004019187/Al

; GENERAL INFORMATION:

; APPLICANT: Robert B. Shannon

; APPLICANT: Amir Sherman

; APPLICANT: Trueheart, Joshua

; APPLICANT: Willie, G. Todd

; TITLE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	145.5	5.9	791	7	CF682666	CF682666 CCAQ27TR
2	143.5	5.8	705	5	BQ110832	BQ110832 VD205D08
3	136	5.5	925	7	CO008256	CO008256 EST796591
4	131	5.3	773	7	CF706713	CF706713 CCAFS591
5	130.5	5.3	570	8	AQ397018	AQ397018 mgxb0021J
6	129.5	5.3	1503	5	BH918679	BH918679 AGENCOURT
7	129	5.3	2472	5	CL961584	CL961584 OBIFFCO06
c	127.5	5.2	731	7	CF868238	CF868238 tric014xd
9	127.5	5.2	786	6	CB898308	CB898308 tric014xd

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